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Our laboratory has made the novel observation that cyclin E is overexpressed and present in lower molecular weight (LMW) isoforms in selected breast cancer cells and tumor tissues. In a retrospective analysis of tumor specimens from 403 breast cancer patients, we previously discovered that overexpression of LMW isoforms cyclin E strongly correlated with the development of distant metastases and poor overall survival. With a median follow-up of 4-years 91.7% of breast cancer cases with cyclin E overexpression developed distant metastases compared to 7% of cases without cyclin E overexpression ($p < 0.001$). We also found that in 126 patients with Stage I breast cancer, cyclin E overexpression had a 100% predictive value for the development of metastatic disease. Based on this retrospective work, our goal for this award was to initiate a PROSPECTIVE study assessing the importance of cyclin E overexpression as a negative predictor of outcome in Stage I and II breast cancers. We have been able to accrue over 120 diagnosed with Stage I and II disease, obtained normal and tumor tissue from these patients and subjected them to western blot analysis with cyclin E antibody. We will do follow-up on these patients for the next 3-5 years and correlate the expression of cyclin E to outcome at the end of the follow-up period.

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TABLE OF CONTENTS

Front Cover.....	page 1
SF 298 Report Documentation Page.....	page 2
Table of Contents.....	page 3
Introduction.....	page 4
Body.....	pages 4-6
Key Research Accomplishments.....	pages 6-7
Reportable Outcomes.....	page 8
Conclusions.....	page 8
References.....	pages 8-10
Appendix.....	-

Introduction:

The overall purpose of this 1 year study was to initiate a prospective study assessing the ability of cyclin E as a predictor of poor outcome only in stage I and II node negative breast cancers.

Body:

Despite significant recent advances in understanding the cell biology and molecular genetics of breast cancer, patient prognosis continues to be primarily determined by the pathological extent of disease in the axillary lymph nodes (1). However, approximately 1/3 of women with lymph node-negative breast cancer who do not receive systemic treatment develop disease recurrence while approximately 1/3 of patients with positive lymph nodes will be free of recurrence 10 years after local-regional therapy alone (2, 3). These data highlight the need for more sensitive and specific prognostic factors. Such factors would help to more precisely inform patients and physicians about expected outcomes and allow for better individualization of systemic treatment use.

A number of biological factors have been studied over the past two decades in an attempt to further refine risk categories of breast cancer. Our efforts to find important biological markers in breast cancer have focused on the G1/S checkpoint and how deregulation of this critical phase of the cell cycle affects the virulence and metastatic potential of breast cancer (4-8). We have specifically been interested in cyclin E because of its importance in the regulation of G1 to S transition in normal dividing cells (9, 10). In addition, abnormal overexpression of the cyclin E protein can result in acceleration through G1 (11, 12).

Cyclin E gene is amplified in some breast cancer cell lines (6, 13) and we have shown that this amplification can result in as much as 64-fold overexpression of cyclin E mRNA that is constitutively expressed across all phases of the cell cycle (8, 14). Other investigators have documented a strong correlation between cyclin E overexpression and lack of estrogen receptor expression (5, 15, 16). More important, we and others have found that high cyclin E levels were associated with a significantly increased risk of death and/or relapse from breast cancer (7, 16, 17), although some studies did not show an association (17, 18).

We discovered that some breast cancer cell lines and human breast cancers can express up to 5 lower molecular weight (LMW) isoforms of cyclin E (ranging in size from 34 to 49 kDa), in addition to overexpression of the full-length cyclin E 50 kDa protein (6, 7, 16, 19). We hypothesized that these LMW isoforms are active and that the expression of these isoforms correlates with the stage and prognosis of breast cancer (7, 16, 20, 21). The previous studies that have examined the prognostic importance of cyclin E in breast cancer have used immunohistochemistry (IHC) staining to detect alteration in cyclin E expression (17, 18). The antibodies used in these studies cannot distinguish between the form of cyclin E found in both normal and tumor cells and those forms of the protein that are unique to tumor cells.

We performed a RETROSPECTIVE study to test our hypothesis and to more fully evaluate the clinical importance of LMW forms of cyclin E in breast cancer. For these retrospective analysis we examined tumor specimens from 403 breast cancer patients and observed that A) Cyclin E is a superior and independent prognostic marker for breast cancer as compared to other tumor and cell cycle markers (i.e.: age, estrogen and progesterone receptor status, DNA index, ploidy, proliferation index, lymph node involvement, Her-2, cyclin D1, p21, p27, p16 and pRb). These analyses revealed that breast cancers that overexpress cyclin E have a

91.7% probability ($p < 0.001$) of having poor prognosis over a 48-month average follow up period. B) In addition, we found that cyclin E overexpression in Stage I breast cancer has a 100% predictive value to poor prognosis in our patient population; i.e. twelve patients with Stage I disease (from 126 Stage I patients) overexpressed cyclin E- all 12 patients expired of disease. Cyclin E was NOT altered in any of the remaining 114 Stage I patients. Collectively the results from our retrospective study revealed that cyclin E and its LMW isoforms proved to be the most powerful independent predictor for survival in stage I-III breast cancer.

Based on these findings our one year goal is to initiate a PROSPECTIVE study assessing the ability of cyclin E as a predictor of poor outcome only in Stage I and II node negative breast cancers. We will also examine the activity and immune-complex formation of cyclin E in extracts prepared from freshly resected tumors. Our long term goal is that once patients with deregulated cyclin E expression are identified, they may then be singled out for therapy that is more aggressive than what currently administered to node negative Stage I or II patients.

Specifically, our objectives were to

- 1: To use cyclin E antibody as a prognostic marker for stage I and II breast cancer in a PROSPECTIVE study.
- 2: Examine the cyclin E associated activity and its immune-complex formation with key cell cycle regulators in freshly resected tumor samples.

Results/Key Research Accomplishments:

During the past year we were successful in initiating our prospective analysis.

1. We obtained freshly resected breast tissue samples (50 mg each of normal adjacent and tumor) from 130 patients diagnosed with stage I and Stage II node negative breast tumors were collected and protein were extracted from each sample.

2. Using monoclonal as well as a polyclonal (generated in my laboratory) antibodies to cyclin E we analyzed the alteration of cyclin E on freshly resected tumors by Western blot analysis.
3. We correlated the cyclin E alterations in samples from (b) with the expression of currently used markers such as the Her-2/neu, EGFR, PCNA, p53, p27, and cyclin D1.
4. Protein extracted from freshly resected breast tissue samples (from 1) was subjected to cyclin E associated kinase activity using polyclonal antibodies to cyclin E in immunoprecipitate (IP) assays using Histone H1 and GST-Rb as substrates.
5. Immune-complexes formed between cyclin E, CDK2, p21, and p27 has been assessed by first IPing tumor tissue extracts with cyclin E antibody, followed by Western blot analysis with the aforementioned antibodies.

At the end of this initial year of our study it is premature to know whether the overexpression and increased activity of cyclin E are predictors of poor outcome in breast cancer patients since these patients have to be followed for 3-5 years, post diagnosis. However, we have been able to make some initial conclusions about the study at this point

1. The overexpression of cyclin E was observed in 18-20% of all cases examined. This percent overexpression recapitulates our retrospective analysis.
2. We observed an inverse correlation between overexpression of cyclin E and low expression of p27, indicative of poor prognosis. Reciprocally, in all specimens with low expression of cyclin E, p27 was overexpressed. These observations also recapitulate what is known about the contribution of these 2 factors to predicting poor outcome.
3. The cyclin E overexpression is independent of the node status of the patients-again, recapitulating our retrospective results.

Conclusion/Reportable Outcome:

During the one-year study, we have accomplished the goals set forth by our proposal. We have accrued the desired number of patients and analyzed them for the biomarkers proposed. Our initial analysis reveals that the overexpression of cyclin E occurs in the same number of patients as those observed in our retrospective analysis. We are now in a position to examine the role of such cyclin E overexpression with prognosis.

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